

FOR THE RECORD

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Genetic Variation of Two New STR Loci D2S1399, D16S3391 in a Chinese Population

POPULATION: Han in eastern China

KEYWORDS: forensic science, DNA typing, short tandem repeats, eastern Chinese Han population, population genetics, D2S1399, D16S3391

TABLE 1—Allele frequencies and forensic statistics for two STR loci in eastern Chinese population.

Allele	D2S1399 (n = 106)	Allele	D16S3391 (n = 110)
12	0.018	8	0.028
13	0.177	9	0.165
14	0.091	10	0.085
15	0.191	11	0.137
16	0.123	12	0.335
17	0.168	13	0.179
18	0.114	14	0.071
19	0.073
20	0.018
21	0.023
22	0.005

Either blood samples or buccal swabs were taken from healthy unrelated Han individuals living in Jiangsu, Zhejiang, Anhui Province and Shanghai City after obtaining their informed consent. Genomic DNA was extracted using a Chelex method (1). PCR was performed using 1–30 ng of genomic DNA in a 37.5 μ L final reaction volume. An Eppendorf Mastercycler gradient system was used for amplification. The PCR products were analyzed by non-denaturing polyacrylamide gel electrophoresis and visualized by silver staining (2). Allele designation was established according to the recommendations of the DNA commission of the ISFH (3). Genetic data were analyzed using Powerstats program (4). The genotype distribution was analyzed for Hardy-Weinberg equilibrium following Hou's method (5) and no deviation from Hardy-Weinberg equilibrium was observed.

Table 1 and Table 2 contain the summary of allele frequencies and forensic values for the two STR loci, respectively.

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TABLE 2—Forensic statistics of two STR loci in eastern Chinese population.

Locus	PIC	DP	Pm	CE	H _o
D2S1399	0.850	0.958	0.082	0.554	0.745
D16S3391	0.770	0.924	0.076	0.667	0.821

PIC: (polymorphism information content), DP: (power of discrimination), CE: (power of exclusion), H_o: (observed heterozygosity).

The complete data can be obtained from the authors on request to yuzhengao@suda.edu.cn.

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